

RAW SEQUENCE LISTING

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Application Serial Number: 10/828,837
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/828,837

DATE: 05/31/2005
TIME: 13:50:23

Input Set : A:\Seq List 10-828837.txt
Output Set: N:\CRF4\05312005\J828837.raw

4 <110> APPLICANT: ADVANCED RESEARCH AND TECHNOLOGY INSTITUTE, INC.
5 RICHARD, GREGORY L
6 CATT, DIANA M
8 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR PROMOTING ORAL HEALTH, AND
9 POLYPEPTIDES USEFUL FOR SAME
11 <130> FILE REFERENCE: IU-104
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/828,837
C--> 13 <141> CURRENT FILING DATE: 2004-04-21
13 <150> PRIOR APPLICATION NUMBER: 10/009,004
14 <151> PRIOR FILING DATE: 2001-11-05
16 <150> PRIOR APPLICATION NUMBER: 60/132,312
17 <151> PRIOR FILING DATE: 1999-05-03
19 <150> PRIOR APPLICATION NUMBER: PCT/US00/11992
20 <151> PRIOR FILING DATE: 2000-05-03
22 <160> NUMBER OF SEQ ID NOS: 8
24 <170> SOFTWARE: PatentIn version 3.3
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 11
28 <212> TYPE: PRT
29 <213> ORGANISM: Streptococcus mutans
31 <400> SEQUENCE: 1
33 Met Ser Ser Gln Ala Lys Ala Asn Asn Ile Pro
34 1 5 10
37 <210> SEQ ID NO: 2
38 <211> LENGTH: 11
39 <212> TYPE: PRT
40 <213> ORGANISM: Streptococcus mutans
43 <220> FEATURE:
44 <221> NAME/KEY: UNSURE
45 <222> LOCATION: (8)...(8)
47 <400> SEQUENCE: 2
W--> 49 Met Gln Arg Pro Thr Glu Phe Xaa Glu Asp Lys
50 1 5 10
53 <210> SEQ ID NO: 3
54 <211> LENGTH: 11
55 <212> TYPE: PRT
56 <213> ORGANISM: Streptococcus mutans
58 <400> SEQUENCE: 3
60 Met Ser Arg Gln Ala Lys Ala Val Asn Ile Pro
61 1 5 10
64 <210> SEQ ID NO: 4
65 <211> LENGTH: 11
66 <212> TYPE: PRT

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67 <213> ORGANISM: Streptococcus mutans
 69 <400> SEQUENCE: 4
 71 Met Gln Ser Pro Thr Glu Phe Asn Glu Asp Lys
 72 1 5 10
 75 <210> SEQ ID NO: 5
 76 <211> LENGTH: 2025
 77 <212> TYPE: DNA
 78 <213> ORGANISM: Streptococcus mutans
 81 <220> FEATURE:
 82 <221> NAME/KEY: CDS
 83 <222> LOCATION: (96)..(1103)
 85 <400> SEQUENCE: 5
 86 atagtaaaaa tttttcaaaa aatatattac gtaagtattg ctaaatattt cttttgtgtt 60
 88 tcaatatagg tgaaaaaaa aatgaagga agatt atg aat caa aaa ata gtc 113
 89 Met Asn Gln Lys Ile Val
 90 1 5
 92 gtc att tcg tca ttt tac atg tta ggt gct cat tca ttt tca aag gca 161
 93 Val Ile Ser Ser Phe Tyr Met Leu Gly Ala His Ser Phe Ser Lys Ala
 94 10 15 20
 96 gta tat cat aat gat agg agt gtg aaa ctt atg aaa aga att gat att 209
 97 Val Tyr His Asn Asp Arg Ser Val Lys Leu Met Lys Arg Ile Asp Ile
 98 25 30 35
 100 aat cat caa gca caa cgt ttt tct att cgt aaa tat gca ttt gga gct 257
 101 Asn His Gln Ala Gln Arg Phe Ser Ile Arg Lys Tyr Ala Phe Gly Ala
 102 40 45 50
 104 gca tct gtt tta att ggc tgt gtc ttt ttt cta ggt acc caa aat gtt 305
 105 Ala Ser Val Leu Ile Gly Cys Val Phe Phe Leu Gly Thr Gln Asn Val
 106 55 60 65 70
 108 tct gca caa gag cag gga act caa ttg cca gca agt gaa aac gca gtt 353
 109 Ser Ala Gln Glu Gln Gly Thr Gln Leu Pro Ala Ser Glu Asn Ala Val
 110 75 80 85
 112 gtg aac gtg gct gaa aat tca gtt gct atc agc caa gca gtt gca gat 401
 113 Val Asn Val Ala Glu Asn Ser Val Ala Ile Ser Gln Ala Val Ala Asp
 114 90 95 100
 116 aag gca gca act caa aca act cta aca gaa aca ccc caa gtt gaa gtt 449
 117 Lys Ala Ala Thr Gln Thr Thr Leu Thr Glu Thr Pro Gln Val Glu Val
 118 105 110 115
 120 gag gag aaa gaa agt aag gta aat gct cct gct tta aat gtc gat gac 497
 121 Glu Glu Lys Glu Ser Lys Val Asn Ala Pro Ala Leu Asn Val Asp Asp
 122 120 125 130
 124 aaa ggt gca aaa tcc aaa gaa gat gtg aac cct act att tca aag aca 545
 125 Lys Gly Ala Lys Ser Lys Glu Asp Val Asn Pro Thr Ile Ser Lys Thr
 126 135 140 145 150
 128 gca agt gaa gtg gaa gct tct gca gta act gct act gat act aaa aat 593
 129 Ala Ser Glu Val Glu Ala Ser Ala Val Thr Ala Thr Asp Thr Lys Asn
 130 155 160 165
 132 tca aat cca caa gtc aat gtt gaa act gac tca agt gaa aaa gac gaa 641
 133 Ser Asn Pro Gln Val Asn Val Glu Thr Asp Ser Ser Glu Lys Asp Glu
 134 170 175 180

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136 aat aaa atg gtc acc tcg gct cca gct aag gag act gag gca gaa caa	689
137 Asn Lys Met Val Thr Ser Ala Pro Ala Lys Glu Thr Glu Ala Glu Gln	
138 185 190 195	
140 aat gag aaa gca gtc aga gaa aat ctt atg caa aga caa gct aag gct	737
141 Asn Glu Lys Ala Val Arg Glu Asn Leu Met Gln Arg Gln Ala Lys Ala	
142 200 205 210	
144 gtc tca att cca tcg caa ggc aat tat gtt ttc caa gaa aca act cct	785
145 Val Ser Ile Pro Ser Gln Gly Asn Tyr Val Phe Gln Glu Thr Thr Pro	
146 215 220 225 230	
148 gta aaa aat gca gcc agt atg tcc agc cca acc caa ttt aac ttt gat	833
149 Val Lys Asn Ala Ala Ser Met Ser Ser Pro Thr Gln Phe Asn Phe Asp	
150 235 240 245	
152 aaa gga gat aag gtt ttt tat gat aat gtt tta gaa gcg gat ggg cat	881
153 Lys Gly Asp Lys Val Phe Tyr Asp Asn Val Leu Glu Ala Asp Gly His	
154 250 255 260	
156 caa tgg att agc tat gtg tct tac agt ggt att cgt cgc tat gct cct	929
157 Gln Trp Ile Ser Tyr Val Ser Tyr Gly Ile Arg Arg Tyr Ala Pro	
158 265 270 275	
160 att gct gtg aca att gaa gaa ttg aag caa aaa gaa att gtt cag caa	977
161 Ile Ala Val Thr Ile Glu Glu Leu Lys Gln Lys Glu Ile Val Gln Gln	
162 280 285 290	
164 aat tta ccg gca caa gga acc tat cac ttt act aaa cag cag agc tta	1025
165 Asn Leu Pro Ala Gln Gly Thr Tyr His Phe Thr Lys Gln Gln Ser Leu	
166 295 300 305 310	
168 aaa atg aag cta aac tgt cta gtc cga ccc aat tct cgt ttt aca acg	1073
169 Lys Met Lys Leu Asn Cys Leu Val Arg Pro Asn Ser Arg Phe Thr Thr	
170 315 320 325	
172 gag atc acg ttt ttt atg ata agg ttt tag aagcggatgg acatcaatgg	1123
173 Glu Ile Thr Phe Phe Met Ile Arg Phe	
174 330 335	
176 attagctatg tgtcctacag tggtatccgt cgttatgttg ttattggaaa gcttacgaca	1183
178 caaccctctc caattgaaac taaagtatca ggtactattt tcatccaaaa taaaacggct	1243
180 caacaattcg atgttgcatt ttctaatgct tcaagcaatc aaggcataaa agaggtatta	1303
182 gtgccagtt ggtcagagca aaacgggcag gatgacattt tctggatca agcaatcaa	1363
184 caaggtaag gcgttataa ggtgaccgtt aagtcagt accataaaaa taatagcggt	1423
186 aactatcatg tccatcttta ttatctttt gataatggtg aacaaagagg agtcggggca	1483
188 acaatgactg aggttggaaagc accagagct gtagaaacaa caggtatcat tagcattgcc	1543
190 aataagagca gccaaggatt tgatgtttt attactaatg cttccagcac tcaagacata	1603
192 aaagaggatt tagtgccggt ttggtcagaa caaaacggac aggacgatat tatttggat	1663
194 caagcaacta aacaaggcga aggcgtttt aaggtggccg ttaaggtcag tgaccataaa	1723
196 aatgacagtg gtaactataa cattcacctt tattatcgcc ttgttaactgg tgaattaaag	1783
198 gttgttggag gaaagacaac gacagttagaa gcccctaata gagcaatctt ccagcacaag	1843
200 gaacttatgt ttctactaat aaagttgagg ttaaaaatga ggccagaaca tctagtccaa	1903
202 ctcagttac cttaataaaa ggagaaagta ttactatga cagtatctt aatgctgatg	1963
204 gacatcaatg gattagctat cgcccttaca gtgttattcg tcgttatatt atcatggtt	2023
206 ga	2025
209 <210> SEQ ID NO: 6	
210 <211> LENGTH: 335	
211 <212> TYPE: PRT	

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212 <213> ORGANISM: Streptococcus mutans
214 <400> SEQUENCE: 6
216 Met Asn Gln Lys Ile Val Val Ile Ser Ser Phe Tyr Met Leu Gly Ala
217 1 5 10 15
220 His Ser Phe Ser Lys Ala Val Tyr His Asn Asp Arg Ser Val Lys Leu
221 20 25 30
224 Met Lys Arg Ile Asp Ile Asn His Gln Ala Gln Arg Phe Ser Ile Arg
225 35 40 45
228 Lys Tyr Ala Phe Gly Ala Ala Ser Val Leu Ile Gly Cys Val Phe Phe
229 50 55 60
232 Leu Gly Thr Gln Asn Val Ser Ala Gln Glu Gln Gly Thr Gln Leu Pro
233 65 70 75 80
236 Ala Ser Glu Asn Ala Val Val Asn Val Ala Glu Asn Ser Val Ala Ile
237 85 90 95
240 Ser Gln Ala Val Ala Asp Lys Ala Ala Thr Gln Thr Thr Leu Thr Glu
241 100 105 110
244 Thr Pro Gln Val Glu Val Glu Glu Lys Glu Ser Lys Val Asn Ala Pro
245 115 120 125
248 Ala Leu Asn Val Asp Asp Lys Gly Ala Lys Ser Lys Glu Asp Val Asn
249 130 135 140
252 Pro Thr Ile Ser Lys Thr Ala Ser Glu Val Glu Ala Ser Ala Val Thr
253 145 150 155 160
256 Ala Thr Asp Thr Lys Asn Ser Asn Pro Gln Val Asn Val Glu Thr Asp
257 165 170 175
260 Ser Ser Glu Lys Asp Glu Asn Lys Met Val Thr Ser Ala Pro Ala Lys
261 180 185 190
264 Glu Thr Glu Ala Glu Gln Asn Glu Lys Ala Val Arg Glu Asn Leu Met
265 195 200 205
268 Gln Arg Gln Ala Lys Ala Val Ser Ile Pro Ser Gln Gly Asn Tyr Val
269 210 215 220
272 Phe Gln Glu Thr Thr Pro Val Lys Asn Ala Ala Ser Met Ser Ser Pro
273 225 230 235 240
276 Thr Gln Phe Asn Phe Asp Lys Gly Asp Lys Val Phe Tyr Asp Asn Val
277 245 250 255
280 Leu Glu Ala Asp Gly His Gln Trp Ile Ser Tyr Val Ser Tyr Ser Gly
281 260 265 270
284 Ile Arg Arg Tyr Ala Pro Ile Ala Val Thr Ile Glu Glu Leu Lys Gln
285 275 280 285
288 Lys Glu Ile Val Gln Gln Asn Leu Pro Ala Gln Gly Thr Tyr His Phe
289 290 295 300
292 Thr Lys Gln Gln Ser Leu Lys Met Lys Leu Asn Cys Leu Val Arg Pro
293 305 310 315 320
296 Asn Ser Arg Phe Thr Thr Glu Ile Thr Phe Phe Met Ile Arg Phe
297 325 330 335
300 <210> SEQ ID NO: 7
301 <211> LENGTH: 1836
302 <212> TYPE: DNA
303 <213> ORGANISM: Streptococcus mutans
306 <220> FEATURE:

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307 <221> NAME/KEY: CDS
308 <222> LOCATION: (1)..(1836)
310 <400> SEQUENCE: 7
311 atg aaa aga att gat att aat cat caa gca caa cgt ttt tct att cgc 48
312 Met Lys Arg Ile Asp Ile Asn His Gln Ala Gln Arg Phe Ser Ile Arg
313 1 5 10 15
315 aaa tat gca ttt gga gct gca tct gtt tta att ggc tgt gtc ttt ttt 96
316 Lys Tyr Ala Phe Gly Ala Ala Ser Val Leu Ile Gly Cys Val Phe Phe
317 20 25 30
319 cta ggt acc caa aat gtt tct gca caa gag cag gga act caa ttg cca 144
320 Leu Gly Thr Gln Asn Val Ser Ala Gln Glu Gln Gly Thr Gln Leu Pro
321 35 40 45
323 gca agt gaa aac gca gtt gtg aac gtg gct gaa aat tca gtt gct atc 192
324 Ala Ser Glu Asn Ala Val Val Asn Val Ala Glu Asn Ser Val Ala Ile
325 50 55 60
327 agc caa gca gtt tca gat aag gca gca gct caa aca act cta aca gaa 240
328 Ser Gln Ala Val Ser Asp Lys Ala Ala Gln Thr Thr Leu Thr Glu
329 65 70 75 80
331 aca ccc caa gtt gaa gtt gag gag aaa gaa aat aag gta aat gct cct 288
332 Thr Pro Gln Val Glu Val Glu Glu Lys Glu Asn Lys Val Asn Ala Pro
333 85 90 95
335 gct tta aat gtc gat gac aaa ggt gca aaa tcc aaa gaa gat gtg aac 336
336 Ala Leu Asn Val Asp Asp Lys Gly Ala Lys Ser Lys Glu Asp Val Asn
337 100 105 110
339 cct act gtt tca aag aca gca agt gaa gtg gaa gct tct gca gta act 384
340 Pro Thr Val Ser Lys Thr Ala Ser Glu Val Glu Ala Ser Ala Val Thr
341 115 120 125
343 gct act gat act aaa aat tca aat cca caa gtc aat gtt gaa act gac 432
344 Ala Thr Asp Thr Lys Asn Ser Asn Pro Gln Val Asn Val Glu Thr Asp
345 130 135 140
347 tca aat gaa aaa gac gaa aat aaa atg gtc acc tcg gct cca gct aag 480
348 Ser Asn Glu Lys Asp Glu Asn Lys Met Val Thr Ser Ala Pro Ala Lys
349 145 150 155 160
351 gag act gag gca gaa caa aat gag aaa gcg gta gca gaa aat ctt atg 528
352 Glu Thr Glu Ala Glu Gln Asn Glu Lys Ala Val Ala Glu Asn Leu Met
353 165 170 175
355 caa aga caa gct aag gct gtc tca att cca tcg caa ggc aat tat gtt 576
356 Gln Arg Gln Ala Lys Ala Val Ser Ile Pro Ser Gln Gly Asn Tyr Val
357 180 185 190
359 ttc caa gaa aca act cct gta aaa aat gca gcc agt atg tcc agc cca 624
360 Phe Gln Glu Thr Thr Pro Val Lys Asn Ala Ala Ser Met Ser Ser Pro
361 195 200 205
363 acc caa ttt aac ttt gat aaa gga gat aag gtt ttt tat gat aag gtt 672
364 Thr Gln Phe Asn Phe Asp Lys Gly Asp Lys Val Phe Tyr Asp Lys Val
365 210 215 220
367 tta gaa gcg gat ggg cat caa tgg att agc tat gtg tct tac agt ggt 720
368 Leu Glu Ala Asp Gly His Gln Trp Ile Ser Tyr Val Ser Tyr Ser Gly
369 225 230 235 240
371 att cgt cgc tat gct cct att gct gtg aca att gaa gaa ttg aag caa 768

RAW SEQUENCE LISTING ERROR SUMMARY
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Input Set : A:\Seq List 10-828837.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:2; Xaa Pos. 8

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/828,837

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Input Set : A:\Seq List 10-828837.txt
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L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:49 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:2
L:49 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0